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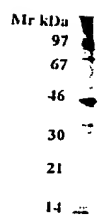
APPROVED	O. FIG.	
BY	CLASS	SUBCLASS
435	435	226

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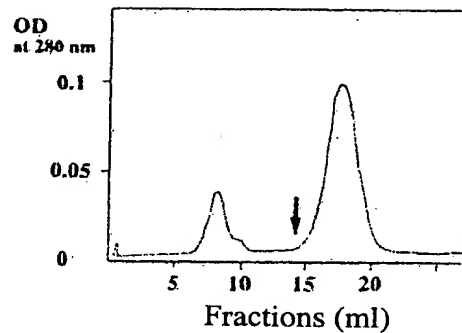
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Figure 1

A

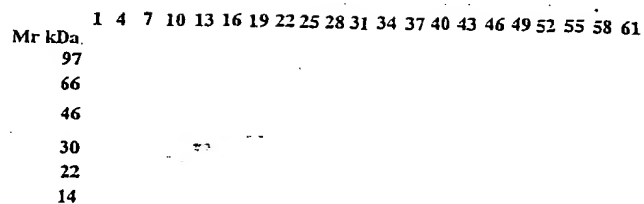


C



B

Fractions



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Figure 2

Protease	-	+	+	+	+	+	-	+	+	+
EDTA	-	+	-	-	-	-	-	-	-	-
CDR-ABC	-	-	+	-	-	-	-	-	-	-
CPI	-	-	-	+	-	-	-	-	-	-
	1	2	3	4	5	6	7	8	9	10

Mr kDa



46

22

14

6.5

3.4

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Figure 3

agaaaattgctgttggg

18 ATG AAG CTT TGC AGC CTT GCA GTC CTT GTA CCC ATT GTT CTC TTC TGT GAG CAG CAT GTC TTC GCG
M K L C S L A V L V P I V L F C E Q H V F A 22

84 TTC CAG AGT GGC CAA GTT CTA GCT GCT CTT CCT AGA ACC TCT AGG CAA GTT CAA GTT CTA CAG AAT
F Q S G Q V L A A L P R T S R Q V Q V L Q N 44

150 CTT ACT ACA ACA TAT GAG ATT GTT CTC TGG CAG CCG GTA ACA GCT GAC CTT ATT GTG AAG AAA AAA
L T T T Y E I V L W Q P V T A D L I V K K K 66

216 CAA GTC CAT TTT TTT GTA AAT GCA TCT GAT GTC GAC AAT GTG AAA GCC CAT TTA AAT GTG AGC GGA
Q V H F F V N A S D V D N V K A H L N V S G 88

282 ATT CCA TGC AGT GTC TTG CTG GCA GAC GTG GAA GAT CTT ATT CAA CAG CAG ATT TCC AAC GAC ACA
I P C S V L L A D V E D L I Q Q Q I S N D T 110

348 GTC AGC CCC CGA GCC TCC GCA TCG TAC TAT GAA CAG TAT CAC TCA CTA AAT GAA ATC TAT TCT TGG
V S P R A S A S Y Y E Q Y H S L N E I Y S W 132

414 ATA GAA TTT ATA ACT GAG AGG CAT CCT GAT ATG CTT ACA AAA ATC CAC ATT GGA TCC TCA TTT GAG
I E F I T E R H P D M L T K I H I G S S F E 154

480 AAG TAC CCA CTC TAT GTT TTA AAG GTT TCT GGA AAA GAA CAA ACA GCC AAA AAT GCC ATA TGG ATT
K Y P L Y V L K V S G K E Q T A K N A I W I 176

546 GAC TGT GGA ATC CAT GCC AGA GAA TGG ATC TCT CCT GCT TTC TGC TTG TGG TTC ATA GGC CAT AAT
D C G I (H) A (R) (E) W I S P A F C L W F I G H N 198

612 CGA ATG TGG AGA AAG AAC CGT TCT TTC TAT GCG AAC AAT CAT TGC ATC GGA ACA GAC CTG AAT AGC
R M W R K (N) (R) S F Y A N N H C I G T D L N (R) 220

678 AAC TTT GTC TCC AAA CAC TGG TGT GAG GAA GGT GCA TCC AGT TCC TCA TGC TCG GAA ACC TAC TGT
N F A S K H W C E E G A S S S S C S E T Y C 242

744 GGA CTT TAT CCT GAG TCA GAA CCA GAA GTG AAG GCA GTG GCT AGT TTC TTG AGA AGA AAT ATC AAC
G L Y P E S E P E V K A V A S F L R R N I N 264

810 CAG ATT AAA GCA TAC ATC AGC ATG CAT TCA TAC TCC CAG CAT ATA GTG TTT CCA TAT TCC TAT ACA
Q I K A Y I S M (H) (S) (Y) S Q H I V F P Y S Y T 286

876 CGA AGT AAA AGC AAA GAC CAT GAG GAA CTG TCT CTA GTA GCC AGT GAA GCA GTT CGT GCT ATT GAC
R S K S K D H E E L S L V A S E A V R A I E 308

942 AAA ACT AGT AAA AAT ACC AGG TAT ACA CAT GGC CAT GGC TCA GAA ACC TTA TAC CTA GCT CCT GGA
K T S K N T R Y T H G H G S E T L (Y) L A P G 330

1008 GGT GGG GAC GAT TGG ATC TAT GAT TTG GGC ATC AAA TAT TCG TTT ACA TCA AAC CCA CCT GTA GAG
G G (D) D W I Y D L G I K Y S F T S N P P V E 352

1074 AAG CTT TTG CCG CTG TCT CTA AAA TAG ctggcatgtcattaggaatgtttaatgccccctgattttatcattctgctt
K L L P L S L K 360

1152 ccgtatttttaatttactgattccagcaagaccaaattcattgtatcagattatttttaagttttatccgtagttttgataaaagattt

1239 tcctatttccttggttctgtcagagaaccttaataagtgtactttgcccattaaggcagactagggttcatgtctttttaccccttttaa

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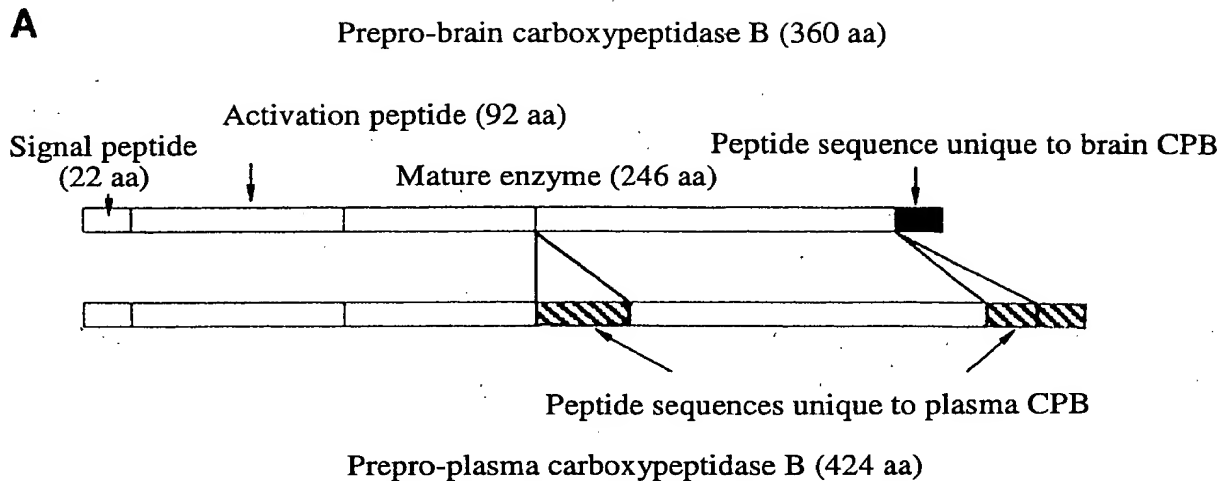
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1500 aaagatttctgctccaaatttttcaataaatttcttctctcttttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

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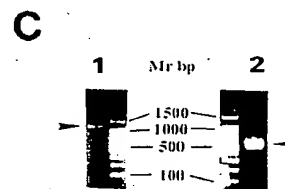
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Figure 4



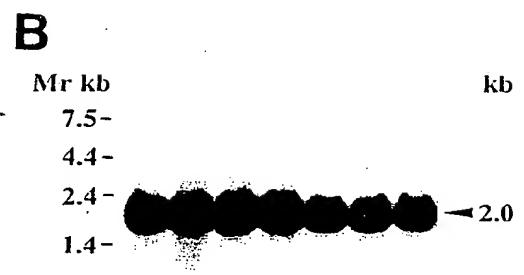
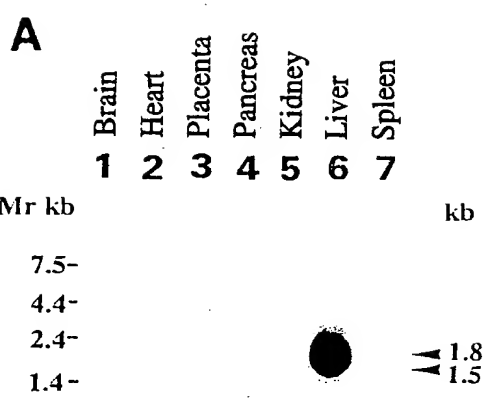
B

Sequence	SN	PP	VEK	LL	PL	SL	K	C-terminus
HBCP82(347-360)	SN	PP	VEK	LL	PL	SL	K	
atpSr(181-194)	SN	PT	IGT	LL	PL	SP	M	
atpSo(182-195)	SD	PV	IHT	LL	PL	SP	K	
atpC1(182-195)	SE	PV	IHT	LL	PL	SP	K	
atpC2(183-196)	SD	PV	IHT	LL	PL	SP	K	



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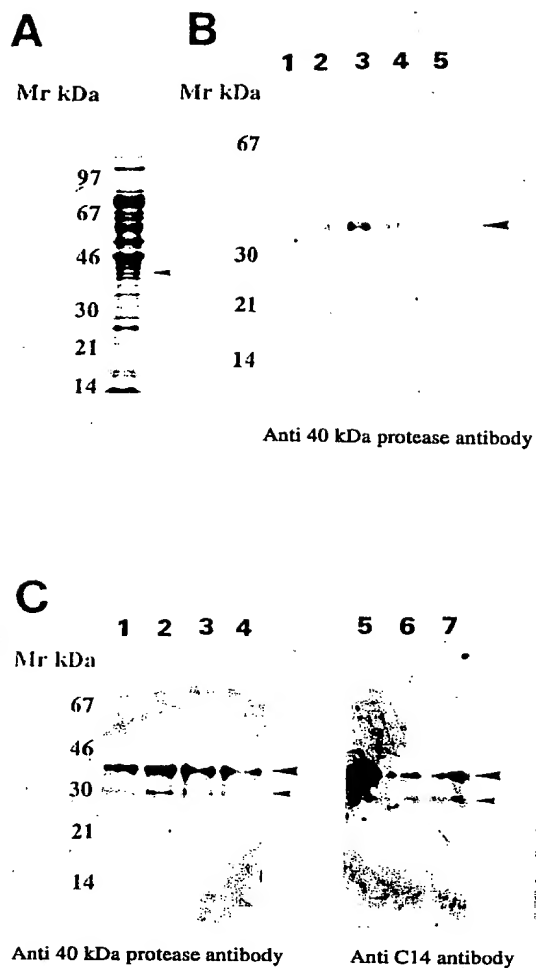
Figure 5



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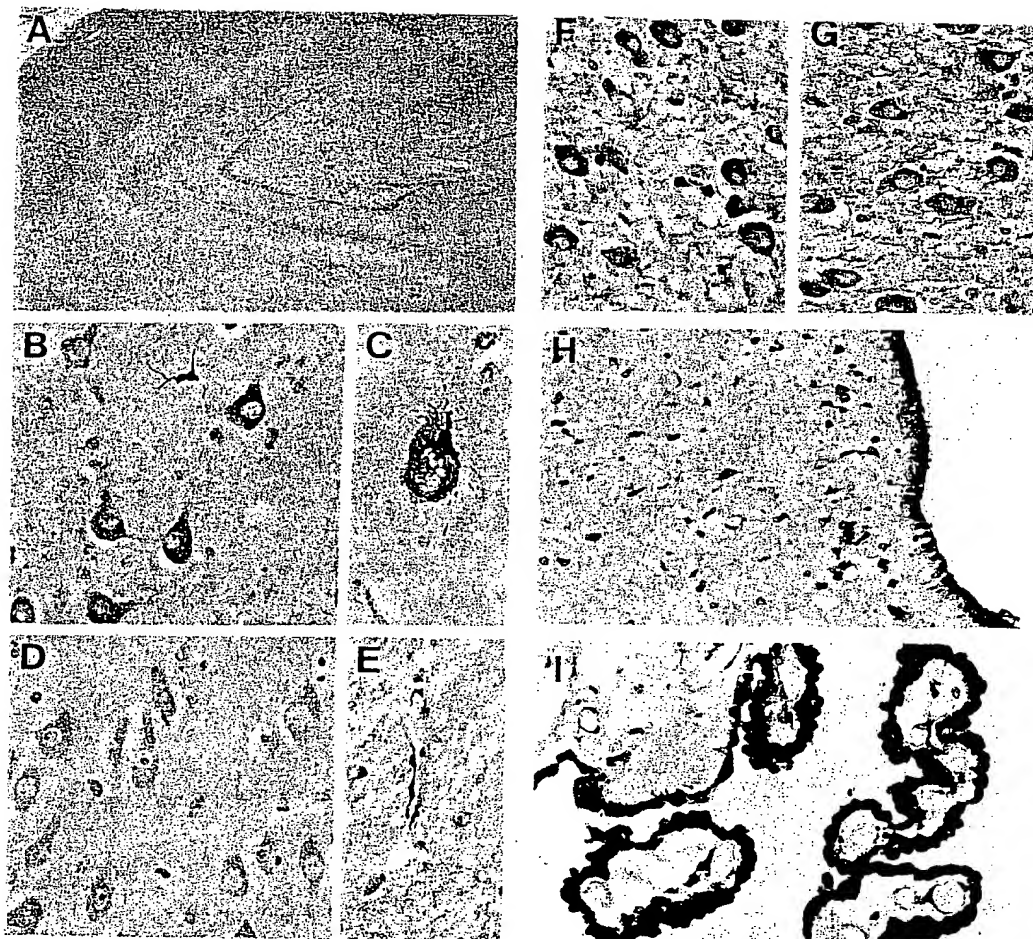
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Figure 6



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Figure 7



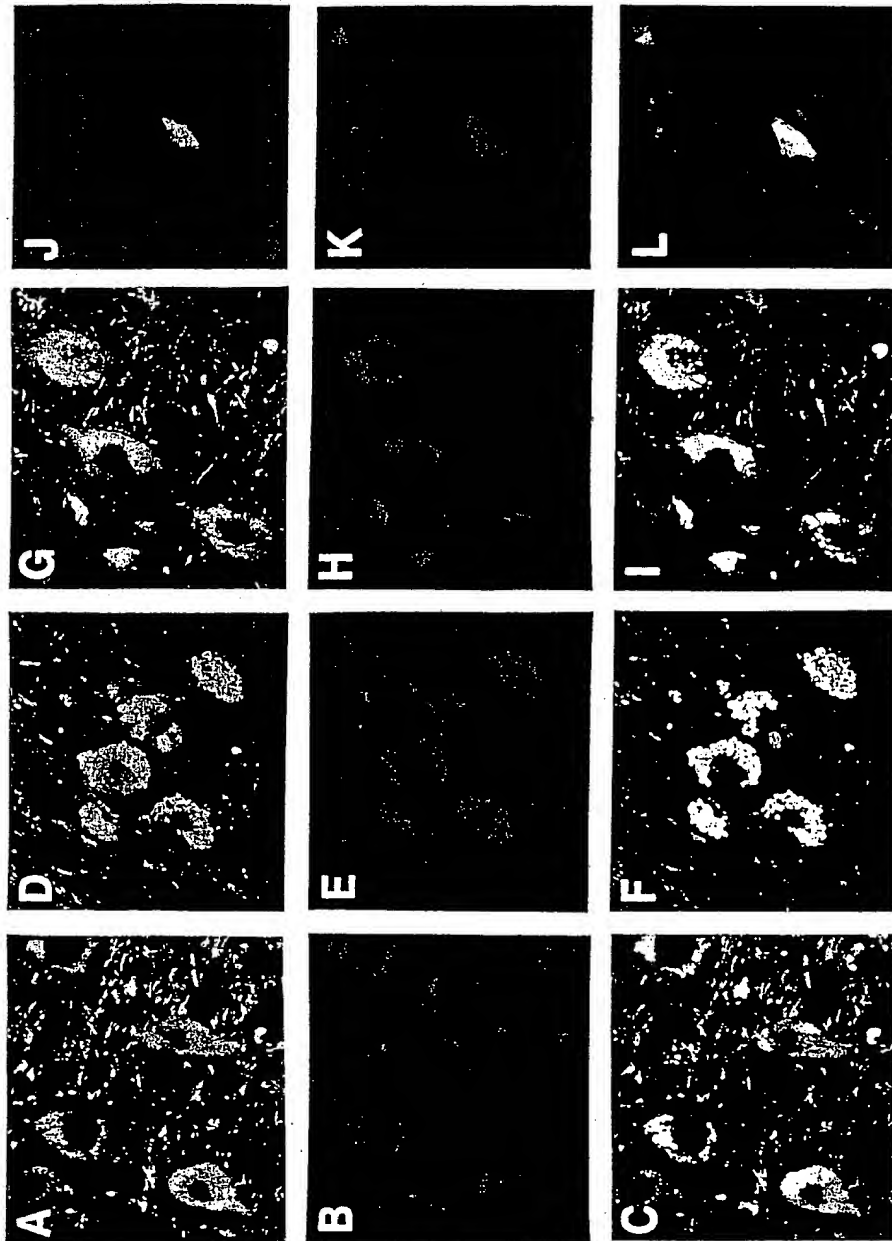
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APPROVED	C. FIG.	
BY	CLASS	SUBCLASS
435	435	220

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Figure 8



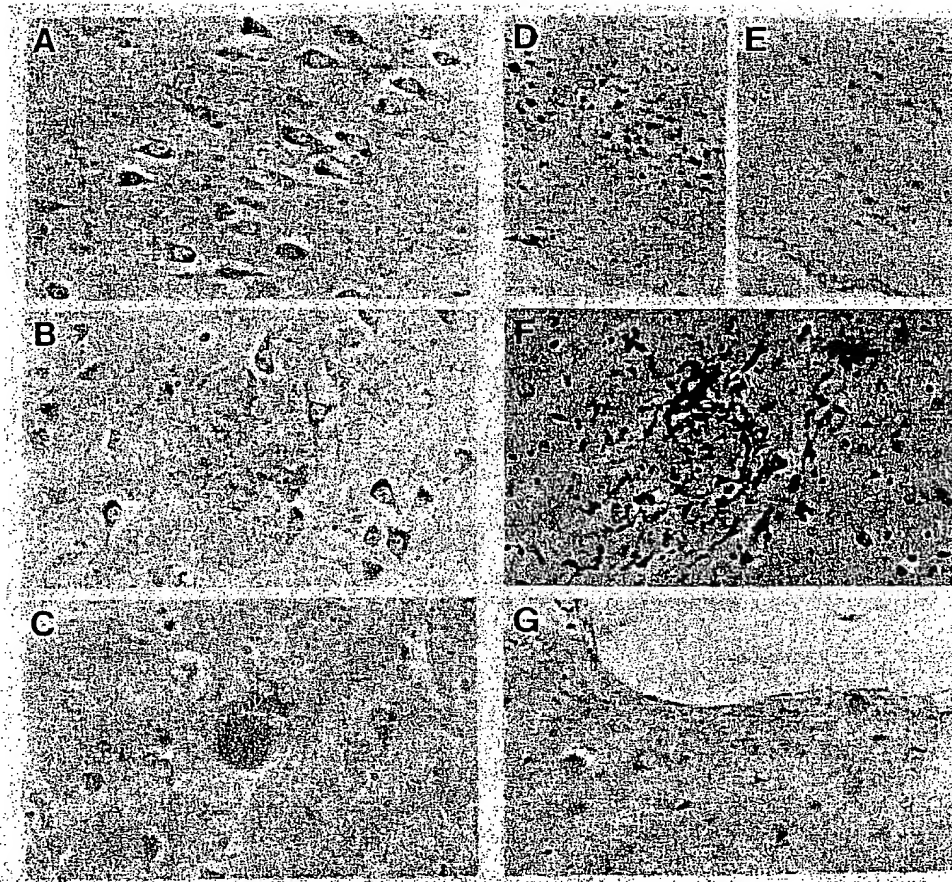
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APPROVED	O. FIG.	
BY	CLASS	SUBCLASS
ROACHMAN	435	226

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Figure 9



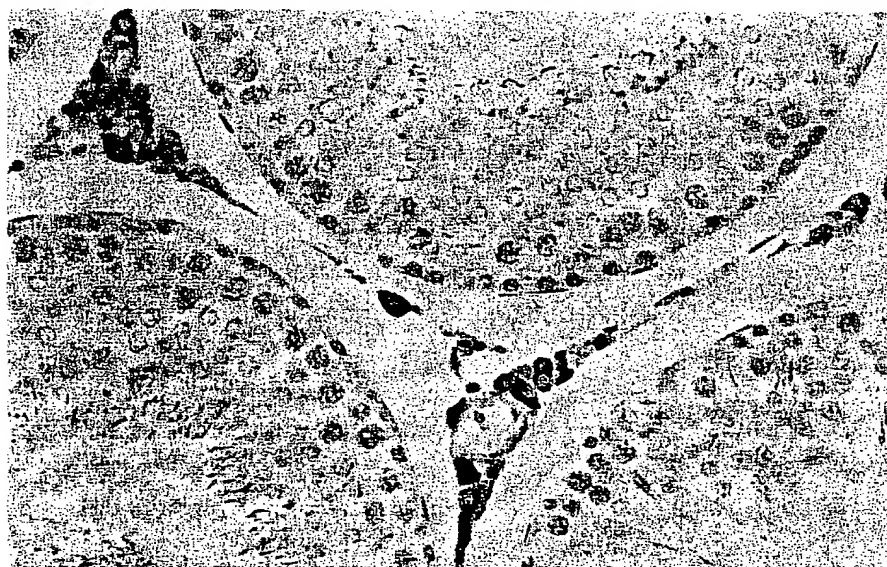
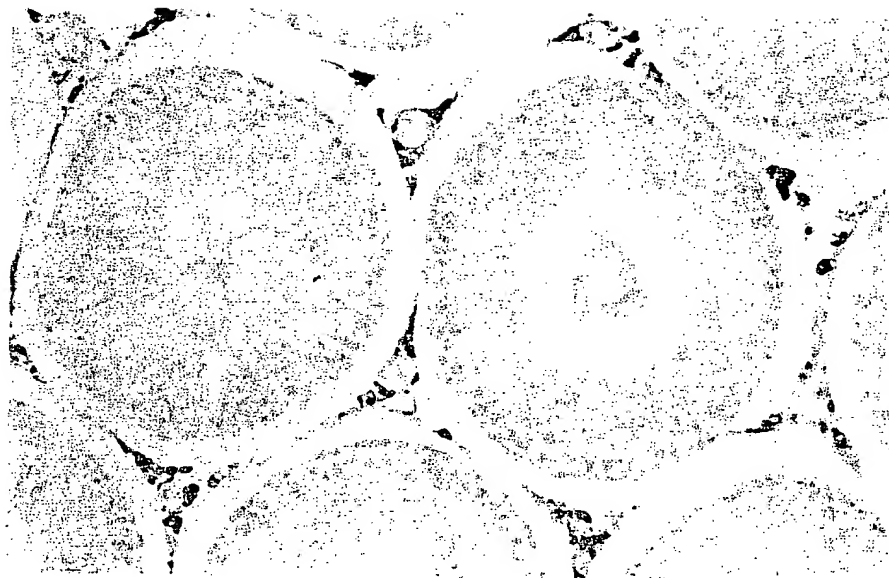
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APPROVED	10	FIG.
BY	CLASS	SUBCLASS
	435	226

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Figure 10



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